

**AMENDMENTS TO THE SPECIFICATION**

Please delete the paragraph on page 10, line 31, to page 11, line 14, and replace it with the following amended paragraph:

**FIGURE 7. Sequence of [f] DEC-205.** (A) Schematic representation of DEC-205. (B) The predicted amino acid sequence of DEC-205 (SEQ ID NO:3) is aligned with the sequences of the bovine PLA2 receptor (SEQ ID NO:4) and the human macrophage mannose receptor (SEQ ID NO:5). Amino acid positions where there is identity among all three proteins are shaded. Protein domains are separated, and consensus amino acids that define C-type CRDs (Weis et al., Science 254:1608-15) are indicated below the relevant sequence as follows: invariant amino acids are shown in single letter code,  $\theta$  = aliphatic,  $\chi$  = aliphatic or aromatic,  $\Phi$  = aromatic, Z = E or Q, B = D or N,  $\Omega$  = D, N, E, or Q. The two missing cysteines in CRD 8 are highlighted with a \*. The consensus sequences ' $\Phi\theta G\theta\Omega\Omega$ ', ' $E\Omega C\theta$ ', ' $\Phi\theta G\theta$ ', 'ZPBB', ' $\Phi\theta G\theta\Omega$ ' and ' $E\Omega C\theta\chi$ ' are disclosed as SEQ ID NOS 7-12, respectively. Peptide sequences determined by automated Edman degradation from purified DEC-205 protein are overlined and numbered (N indicates amino terminal, T indicates peptides generated with Trypsin, and L indicates peptides generated with endoproteinase lys-C). (C) Comparison of carboxyl-terminal cytoplasmic domain sequences of human (*top*) (SEQ ID NO:1) and murine (*bottom*) (SEQ ID NO:6) DEC-205. Regions of identity are underlined; regions of similarity are italicized.